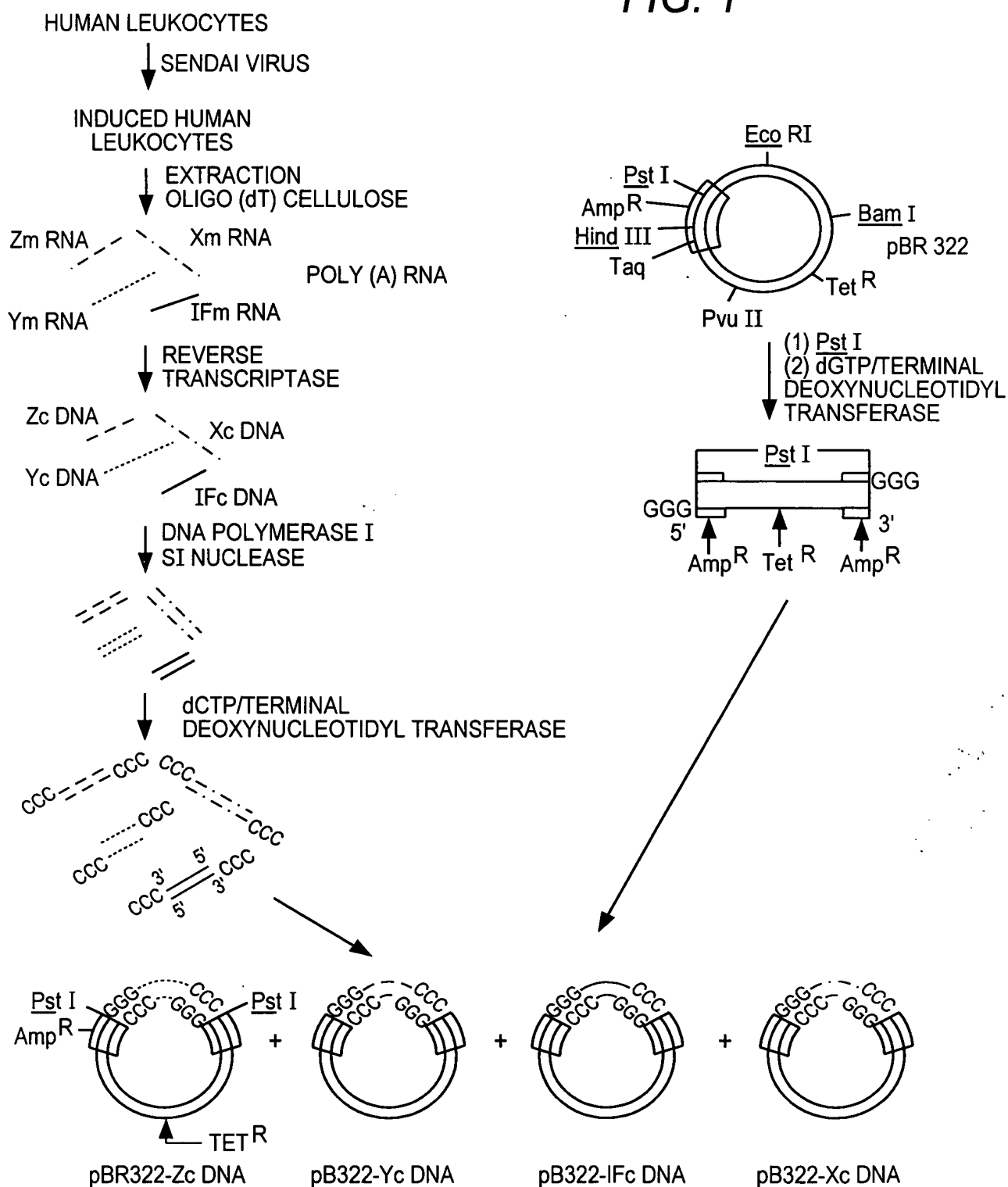




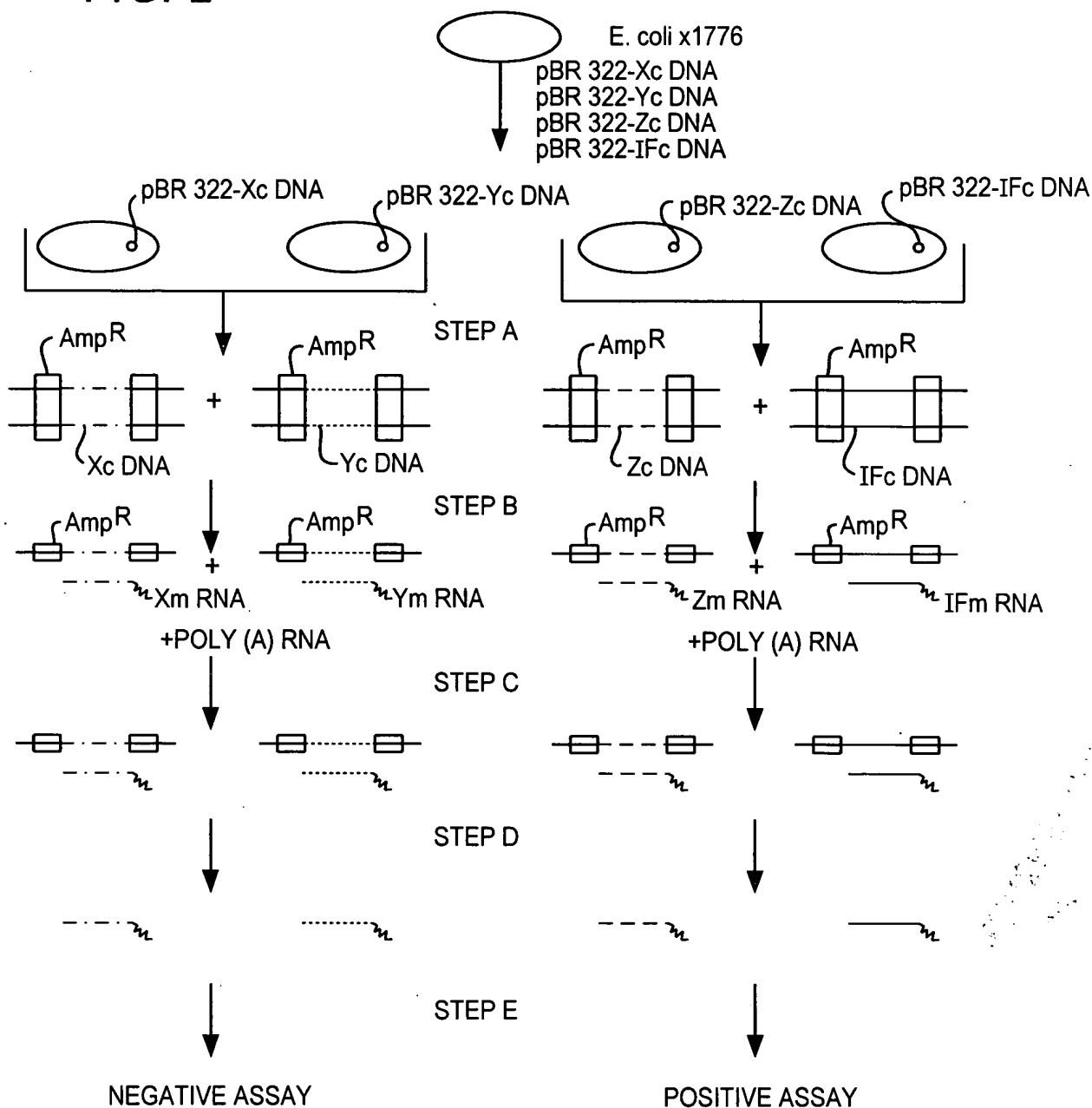
FIG. 1





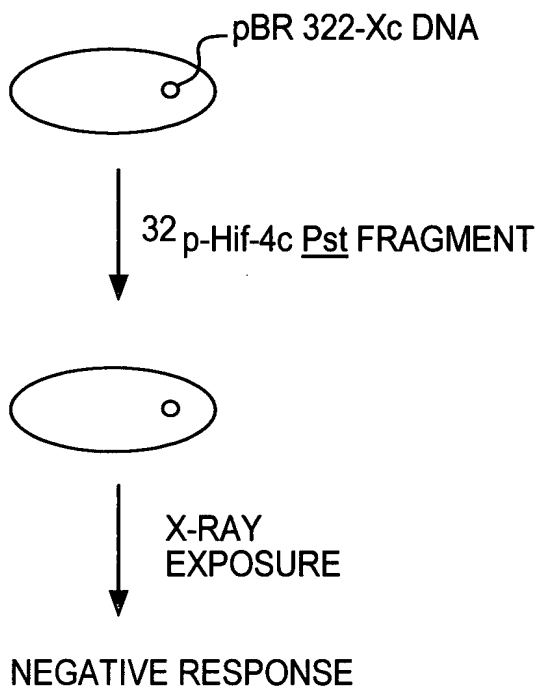
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FIG. 2

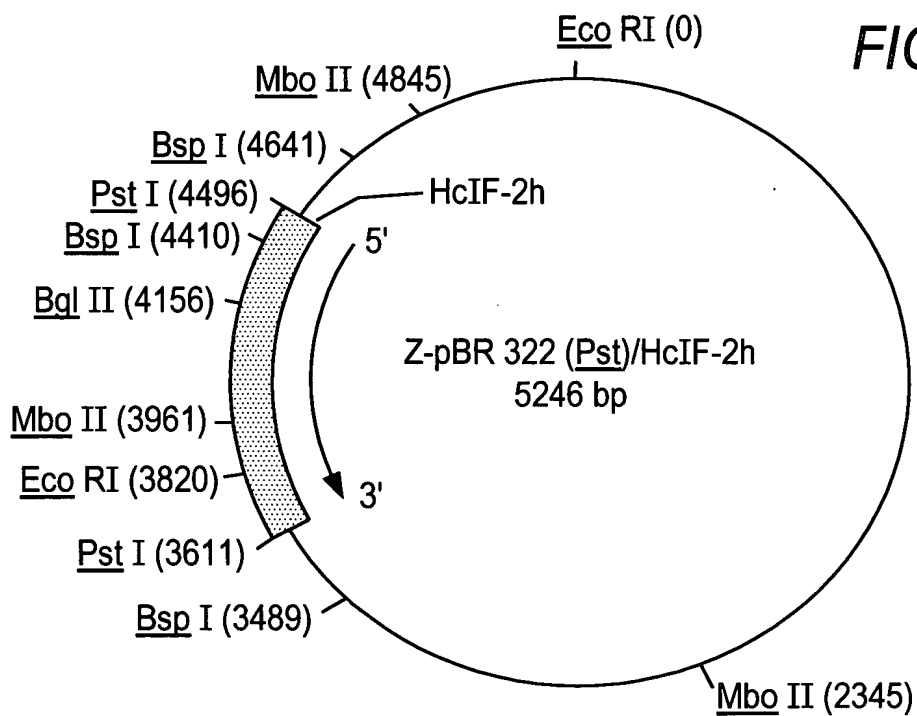
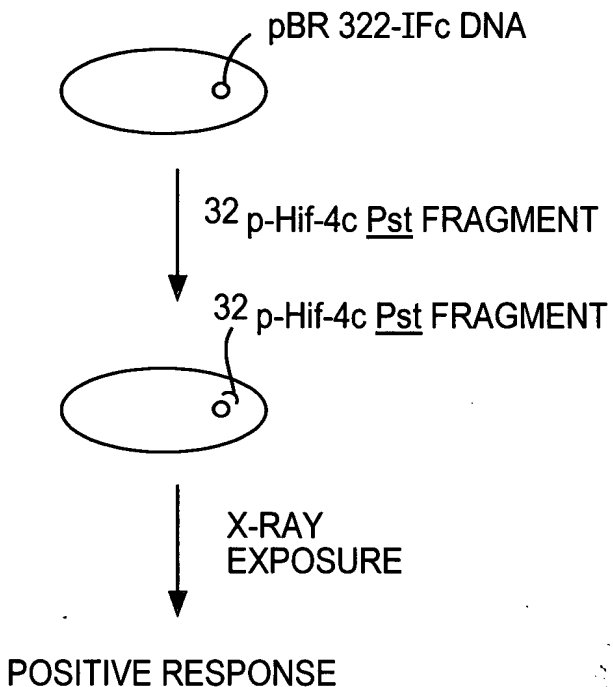




**FIG. 3a**



**FIG. 3b**



**FIG. 4**



FIG. 5a

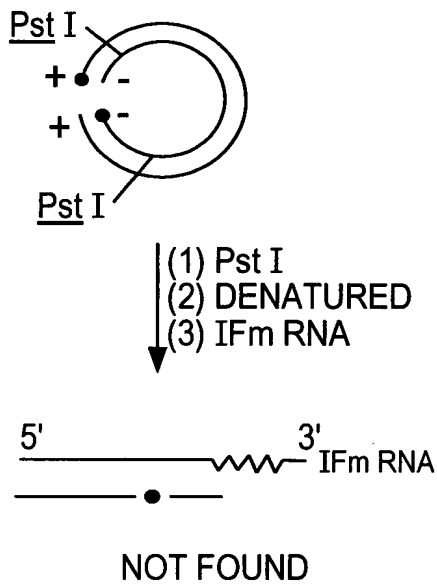
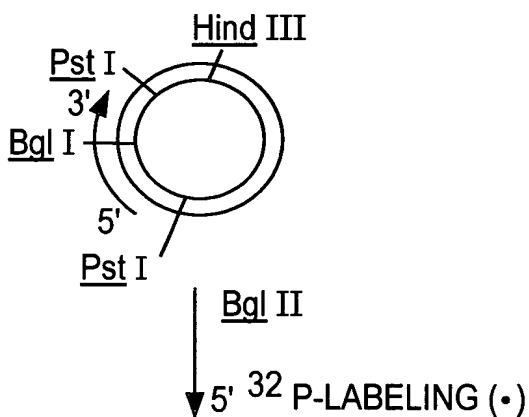
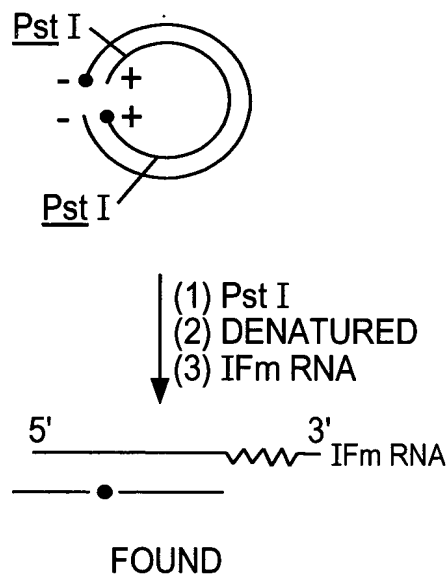
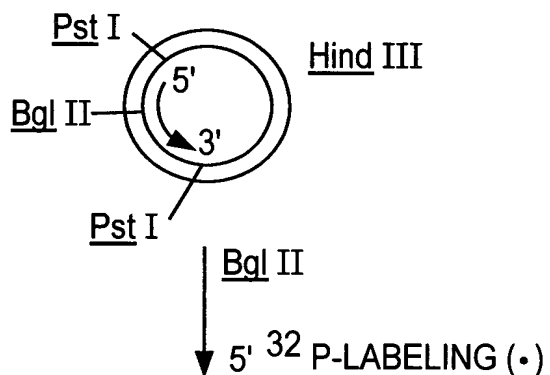


FIG. 5b





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10 20  
MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisProGluThr  
pBR322 ATGAGTATTCAACATTTCCGTGTGCGCCCTTATTCCTTTTTTGGCGCATTTTGGCTCCTGTTTTTGTCTACCCAGAAACG

29 181  
LeuVal ProAlaAlaMet  
CTGGTG ... CCIGCAGCAATG ...  
Pst

24  
MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisArgCysSerAsn  
pKT279 ATGAGTATTCAACATTTCCGTGTGCGCCCTTATTCCTTTTTTGGCGCATTTTGGCTCCTGTTTTTGTCTACCCGCTGCAGCAATG ...  
Pst

25  
MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisProLeuGlnGln ...  
pKT280 ATGAGTATTCAACATTTCCGTGTGCGCCCTTATTCCTTTTTTGGCGCATTTTGGCTCCTGTTTTTGTCTACCCGCTGCAGCAATG ...  
Pst

27  
MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisProGluThr ...  
pKT287 ATGAGTATTCAACATTTCCGTGTGCGCCCTTATTCCTTTTTTGGCGCATTTTGGCTCCTGTTTTTGTCTACCCAGAAACG

AlaAlaAlaMet  
GCTGCAGCAATG ...  
Pst

FIG. 6



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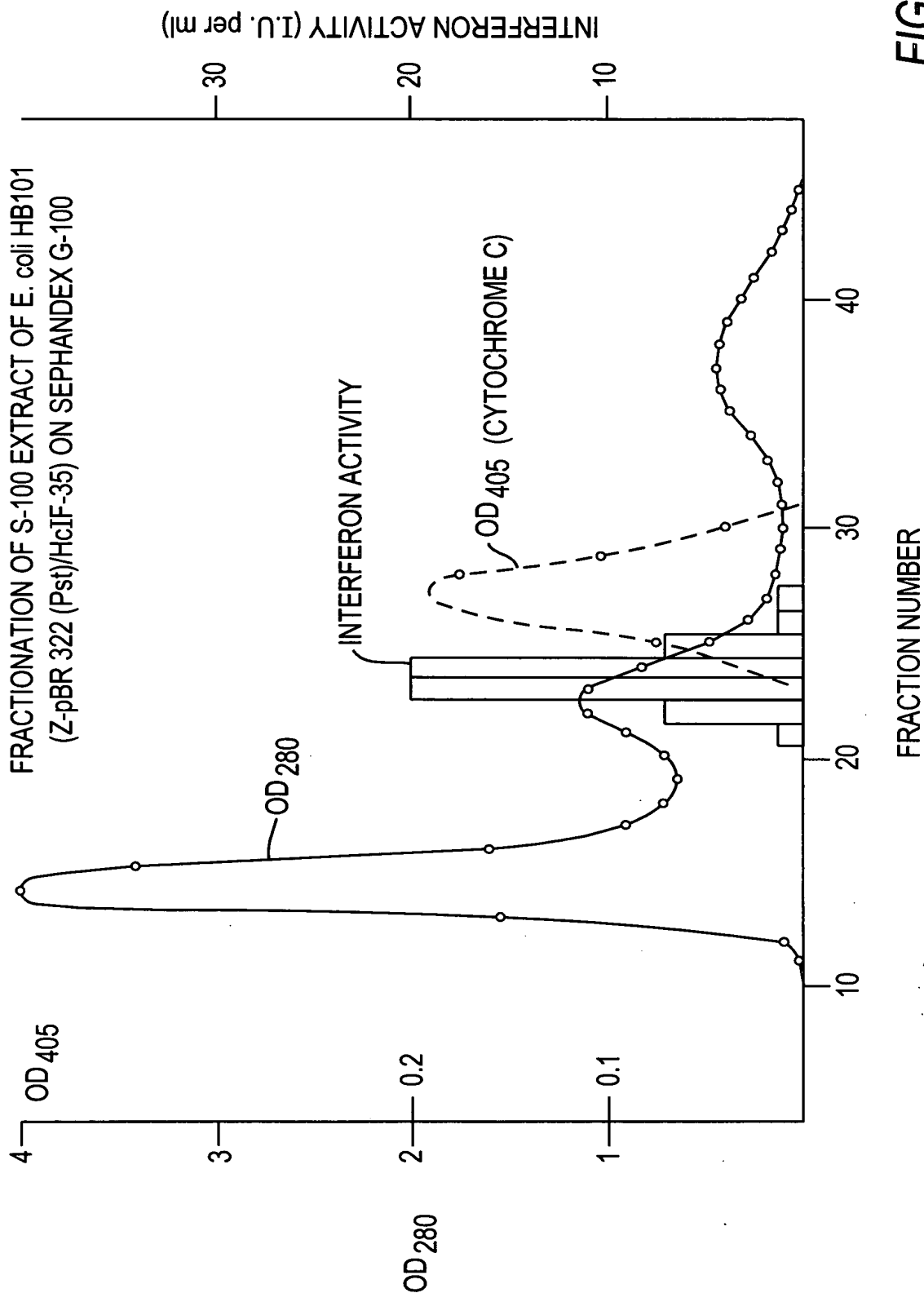


FIG. 7

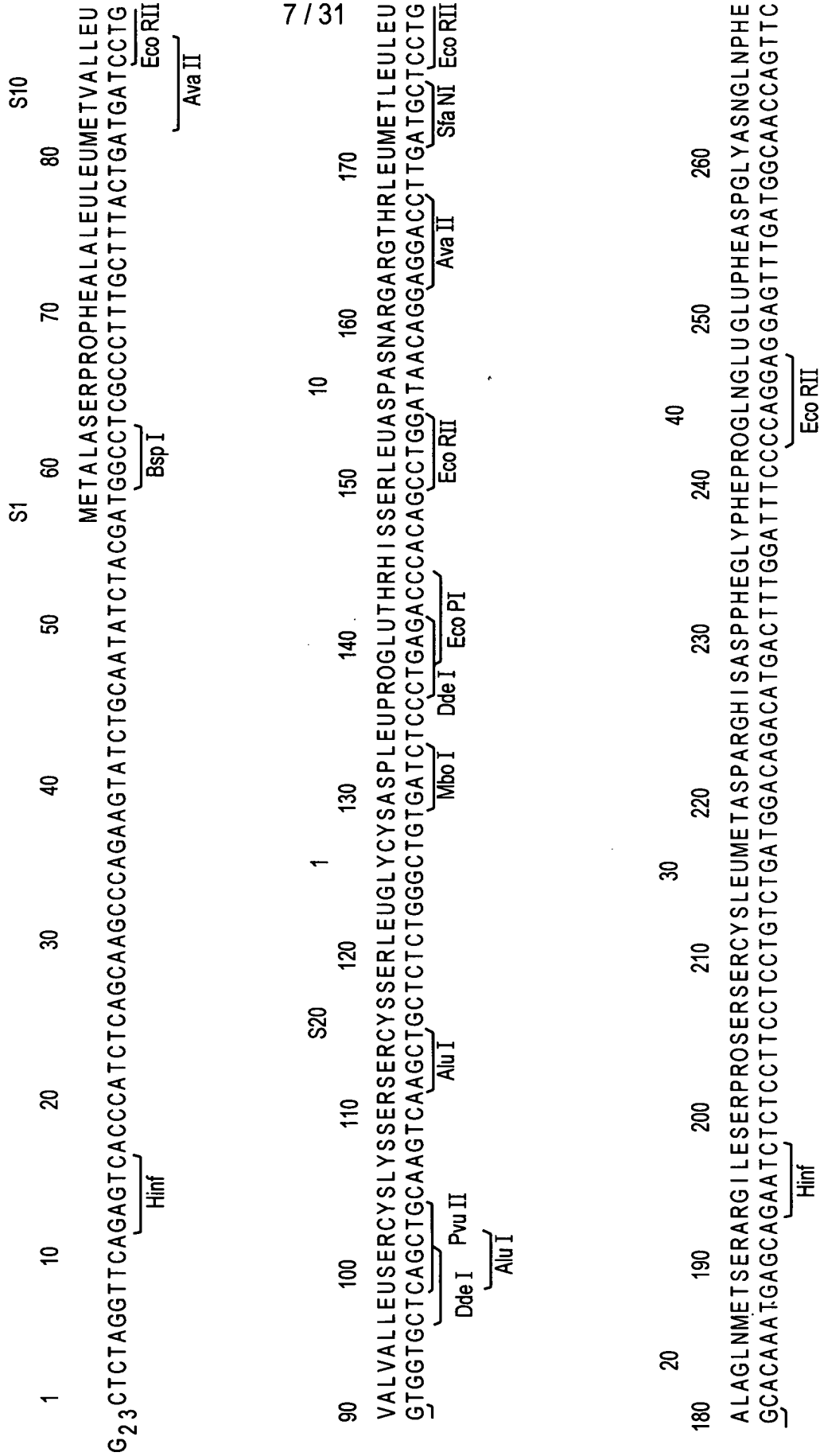


FIG. 8



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50 270 280 290 300 310 320 330 340 350  
G L N L Y S A L P R O A L A I L E S E R V A L L E U H I S G L U L E U I L E G L N L I L E P H E A S N L E U P H E T H R T H R L Y S A S P S E R S E R A L A A L A T R P A S P  
C A G A A G G C T C C A G C C A T C T C T G T C C T C C A T G A G C T G A T C C A G C A G A T C T T C A A C C T C T T T A C C A C A A A G A T T C A T C T G C T G C T T G G G A T  
AluMbo I / EcoP15 Bgl II Mbo I Mbo II Hinf

80 360 370 380 390 400 410 420 430 440  
G L U A S P L E U L E U A S P L Y S P H E C Y S T H R G L U L E U T Y R G L N L E U A S N A S P L E U G L U A L A C Y S V A L M E T G L N G L U G L U A R G V A L G L Y G L U  
G A G G A C C T C C T A G A C A A A T T C T G C A C C G A A C T C T A C C A G C A G C T G A A T G A C T T G G A A G C C T G T G T G A T G C A G G A G A G A G G T G G G A G A A  
Ava I EcoP15 Pvu II Alu I Sfa NI

110 450 460 470 480 490 500 510 520 530  
T H R P R O L E U M E T A S N A L A A S P S E R I L E L E U A L A V A L L Y S L Y S T Y R P H E A R G A R G I L E T H R L E U T Y R L E U T H R G L U L Y S L Y S T Y R S E R P R O  
A C T C C C C T G A T G A A T G C G G A C T C C A T C T T G G C T G T G A A G A A A T A C T T C C G A A G A A T C A C T C T C T A T C T G A C A G A G A A A T A C A G C C C T  
Hinf Mbo II Mbo II Hinf

FIG. 9





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140 150 160 166  
540 550 560 570 580 590 600 610 620  
CYSALATRPGLUVALARGALAGLUILEMETARGSERLEUSERLEUSERTHRASNLEUGLNUARGLEUARGGLYSGLU  
TGTGCCTGGGAGGTGTCAGAGCAGAAATCATGAGATCCCTCTCTTTATCAACAACTTGCAAGAAAGATTAGGAGGAAGGAATAACAT  
EcoRII MboII

630 640 650 660 670 680 690 700 710  
CTGGTCCAACATGAAAACAATTCTTATTGACTCATACACCGGTCACGCTTTTCATGAATTCCTGTCAATTTCAAAGACTCTCACCCCTGCTA  
AvaII Hinf EcoRII EcoRI Hinf Hph

720 730 740 750 760 770 780 790 800  
TAACTATGACCATGCTGATAAACTGATTATCTATTTAAATATTTTAACTATTCATAAGATTTAAATTTTGTTCATATAACGT

810 820 830 840 850 860 865  
CATGTGCACCTTTACACTGTGGTTAGTGTAAATAAACATGTTCCCTTATATTACTCAAAAAAAC<sub>15</sub>  
AccI

FIG. 10



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FIG. 11A

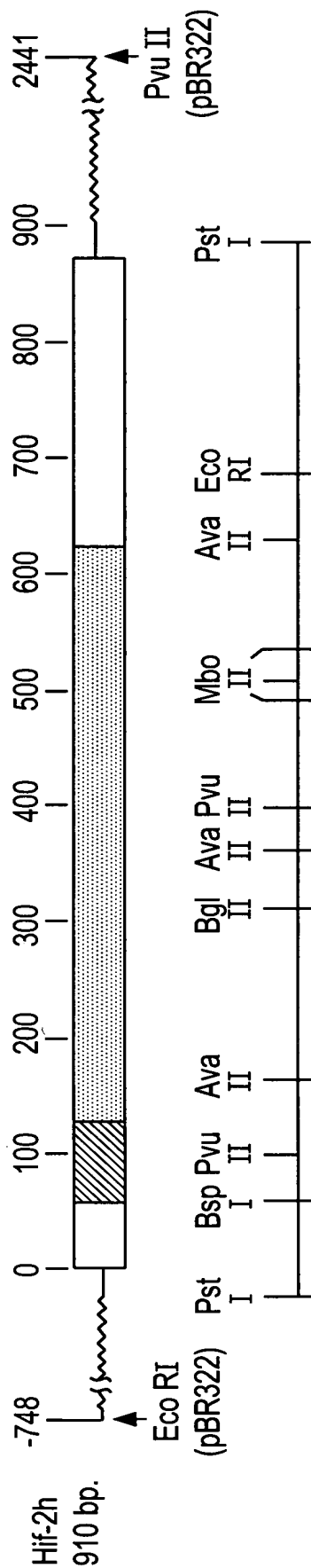
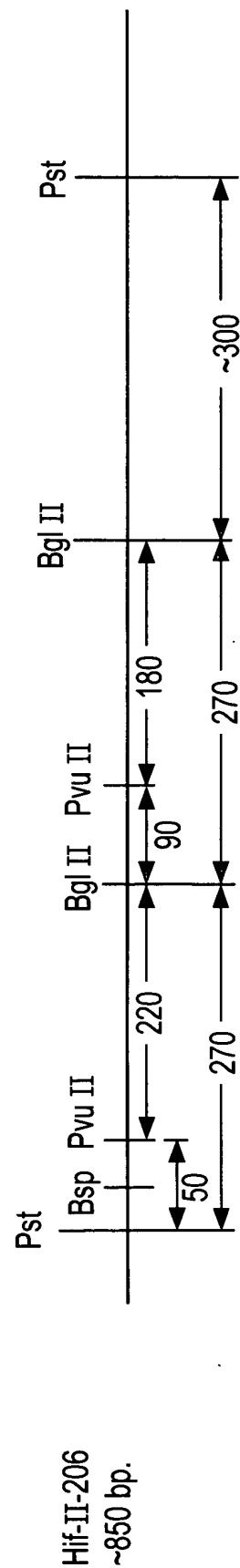


FIG. 11B





206(II)

-50 -40  
G<sub>13</sub>.TTACTGGTGGCCCTC.  
leu leu val ala leu

-20

met ala ser pro phe ala leu leu met val leu  
G<sub>23</sub>CTCTAGGTTACAGTCACCCCATCTCAGCAAGCCCAAGATCTGCAATATCTACGATGGCCCTTGGCCCTTTACTGATGGTCCTG.  
-120 -110 -100 -90 -80 -70 -60 -50 -40

206(II)

CTGGTGCTCAGCTGCAAGTCAAGCTGCCTCTGTGGGCTGTGATCTGCCCTCAAAACCCACAGCCCTGGTAGCAGGAGGACCTTGATGCTCCTG.  
leu val leu ser cys lys ser cys ser val gly cys asp leu pro gln thr his ser leu gly ser arg arg thr leu met leu leu  
-30 -20 -10 -1 10 20 30 40 50

10

-1 1

-10

val val leu ser cys lys ser cys ser leu gly cys asp leu pro glu thr his ser leu asp asn arg arg thr leu met leu leu  
GTGGTGCTCAGCTGCAAGTCAAGCTGCCTCTGTGGGCTGTGATCTCCCTGAGACCCACAGCCCTGGATAACAGGAGGACCTTGATGCTCCTG.  
-30 -20 -10 1 10 20 30 40 50

FIG. 12



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206(II) 60 70 80 90 100 110 120 130 140  
GCACAGATGAGGAGATCTCTCTTTCTCTCGCTTGAAGACAGACATGACCTTGGATTTCCTCCAGGAGGAGTTT---GGCAACCAGTTT.  
2h(I) ALA GLN MET ARG ARG ILE SER LEU PHE SER CYS LEU LYS ASP ARG HIS ASP PHE GLY PHE PRO GLN GLU GLU PHE - GLY ASN GLN PHE

20 30 40  
ALA GLN MET SER ARG ILE SER PRO SER SER CYS LEU MET ASP ARG HIS ASP PHE GLY PHE PRO GLN GLU GLU PHE ASP GLY ASN GLN PHE  
2h(I) GCACAAATGAGCAGAAATCTCTCTCTCTCTCTGCTGATGGACAGACATGACCTTGGATTTCCTCCAGGAGGAGTTTGTATGGCAACCAGTTT.  
60 70 80 90 100 110 120 130 140

206(II) 150 160 170 180 190 200 210 220 230  
CAAAGGCTGAAACCATCCCTGTCTCCATGAGATGATCCAGCAGATCTTCAA TCTCTTCAGCACAAAGGACTCATCTGCTGCTTGGGAT.  
2h(I) GLN LYS ALA GLU THR ILE PRO VAL LEU HIS GLU MET ILE GLN GLN ILE PHE ASN LEU PHE SER THR LYS ASP SER SER ALA ALA TRP ASP  
50 60 70

50 60 70  
GLN LYS ALA PRO ALA ILE SER VAL LEU HIS GLU LEU ILE GLN GLN ILE PHE ASN LEU PHE THR THR LYS ASP SER SER ALA ALA TRP ASP  
2h(I) CAGAAAGGCTCCAGGCATCTCTGTCTCCATGAGCTGATCCAGCAGATCTTCAACCTCTTTACCCACAAAGATTCTCTGCTGCTTGGGAT.  
150 160 170 180 190 200 210 220 230

FIG. 13



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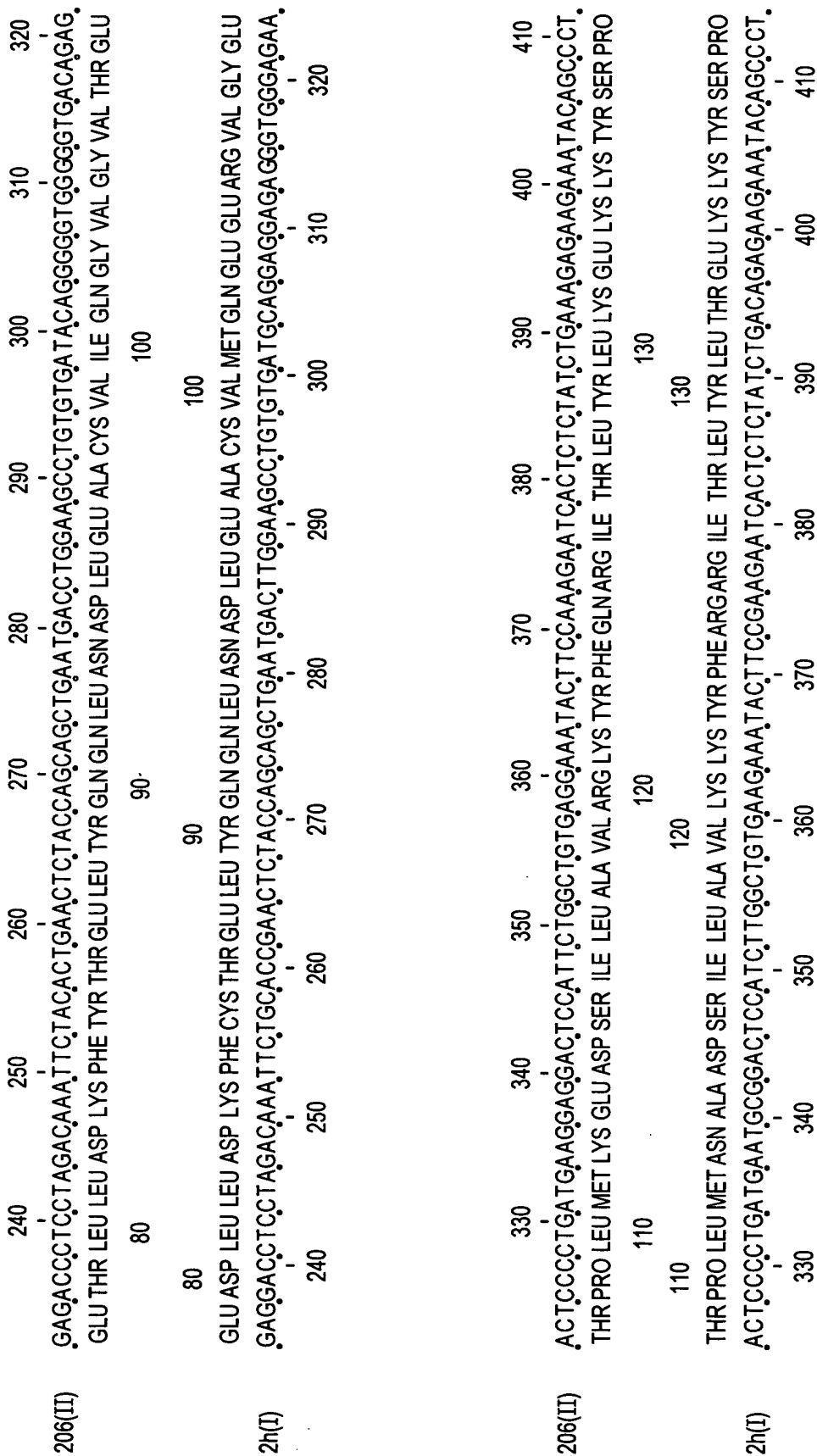


FIG. 14



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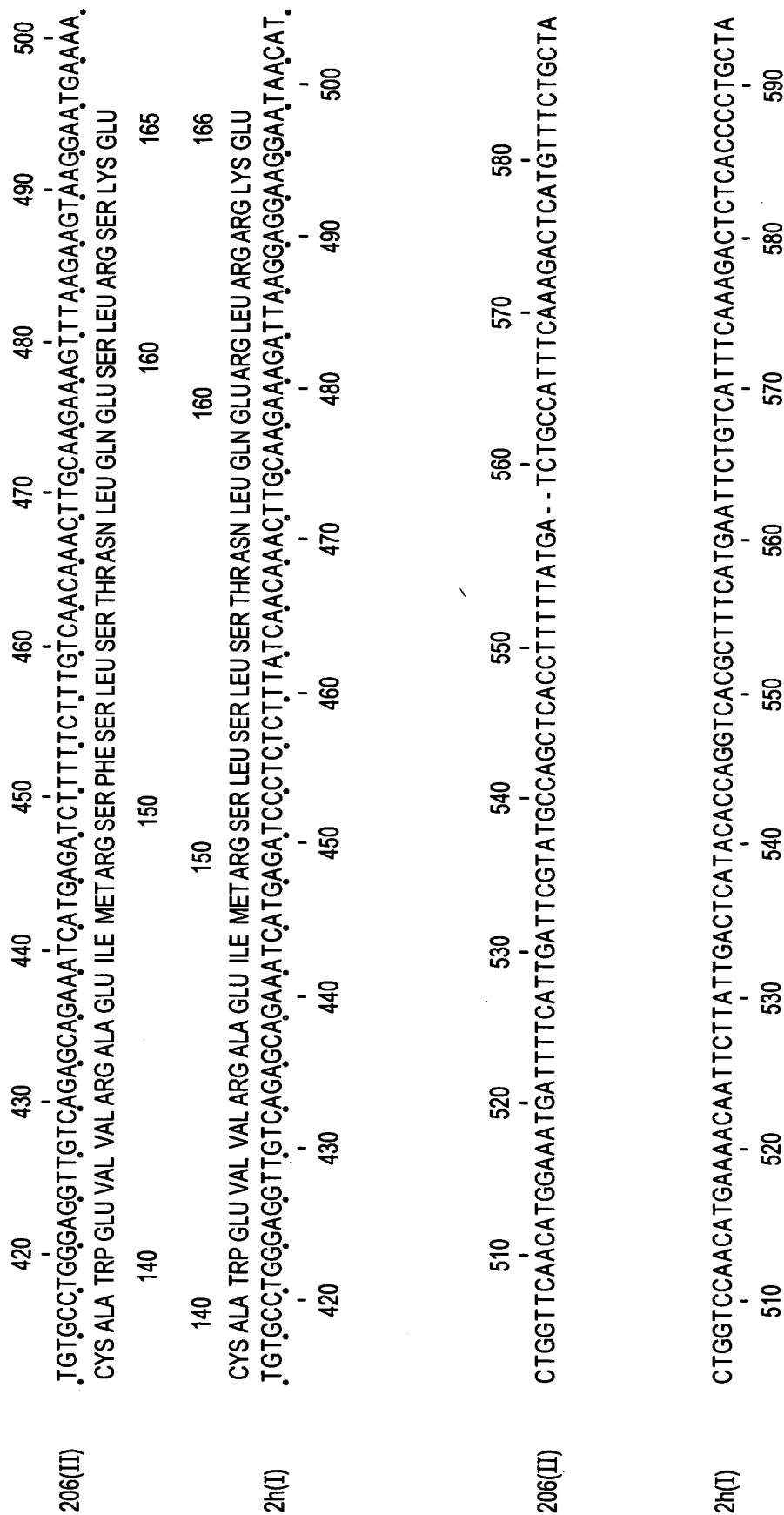


FIG. 15



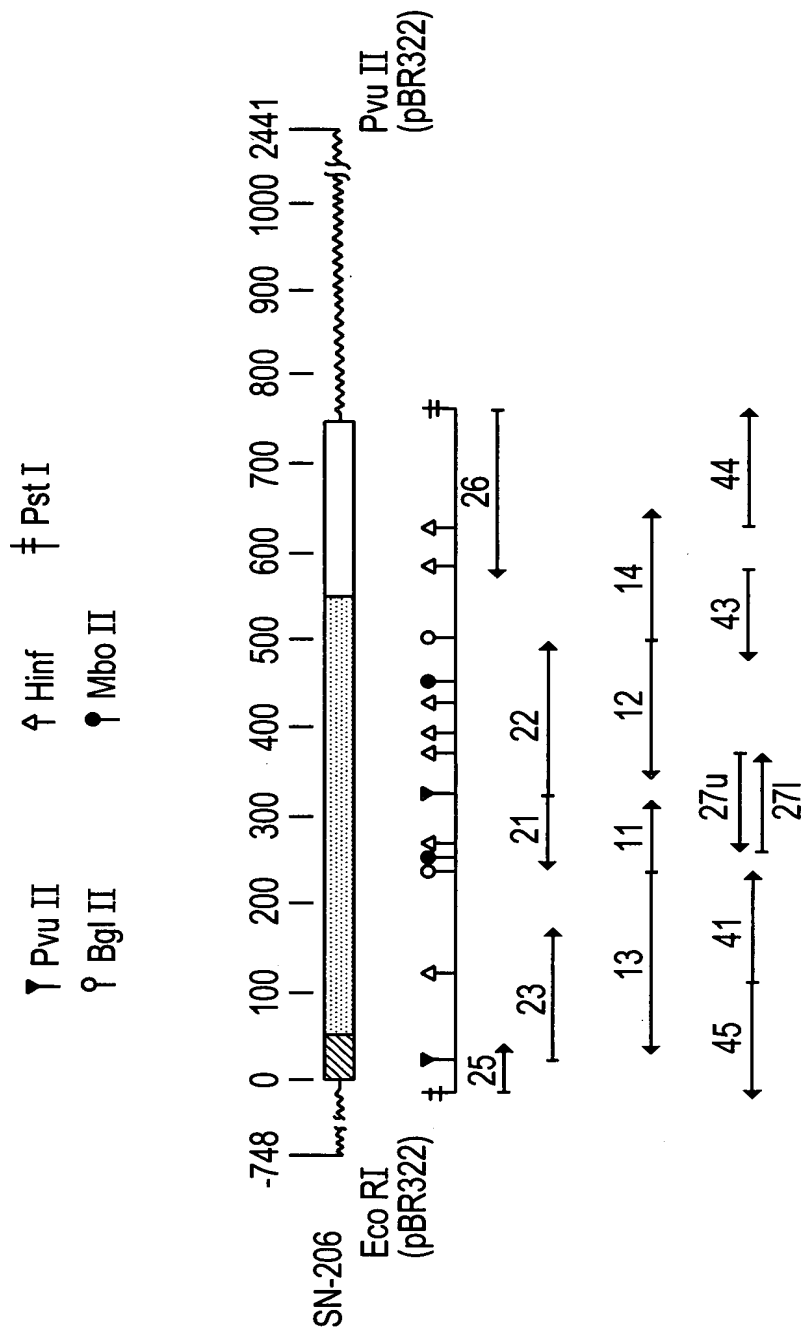
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206(II)	590	TGACCATGACACGATTTAAATCTTTTTCAAATGTTTTTAGGAGTATTAATCAACATTGTATTTCAGCTCTTAAGGCACCTAGTCCCTTACAGAG	680
	600		670
	610		660
	620		650
	630		640
	640		630
	650		620
	660		610
	670		600
	680		590
2h(I)	600	TAACTATGACCATGCTGATAAACTGATTTATCTATTTTAAATATTTTAACTATTCATAAGATTTAAATTTATTTTGTTCATATAACGTC	680
	610		670
	620		660
	630		650
	640		640
	650		630
	660		620
	670		610
	680		600
206(II)	690	GACCATGCTGAC <sub>29</sub>	
	700		
	710		
	720		
	730		
	740		
2h(I)	690	ATGTGCACCTTTACACCTGTGGTTAGTGTAAATAAAACATGTTCCCTTATATTTTACTCAAAAAAAC <sub>15</sub>	
	700		
	710		
	720		
	730		
	740		

FIG. 16



FIG. 17

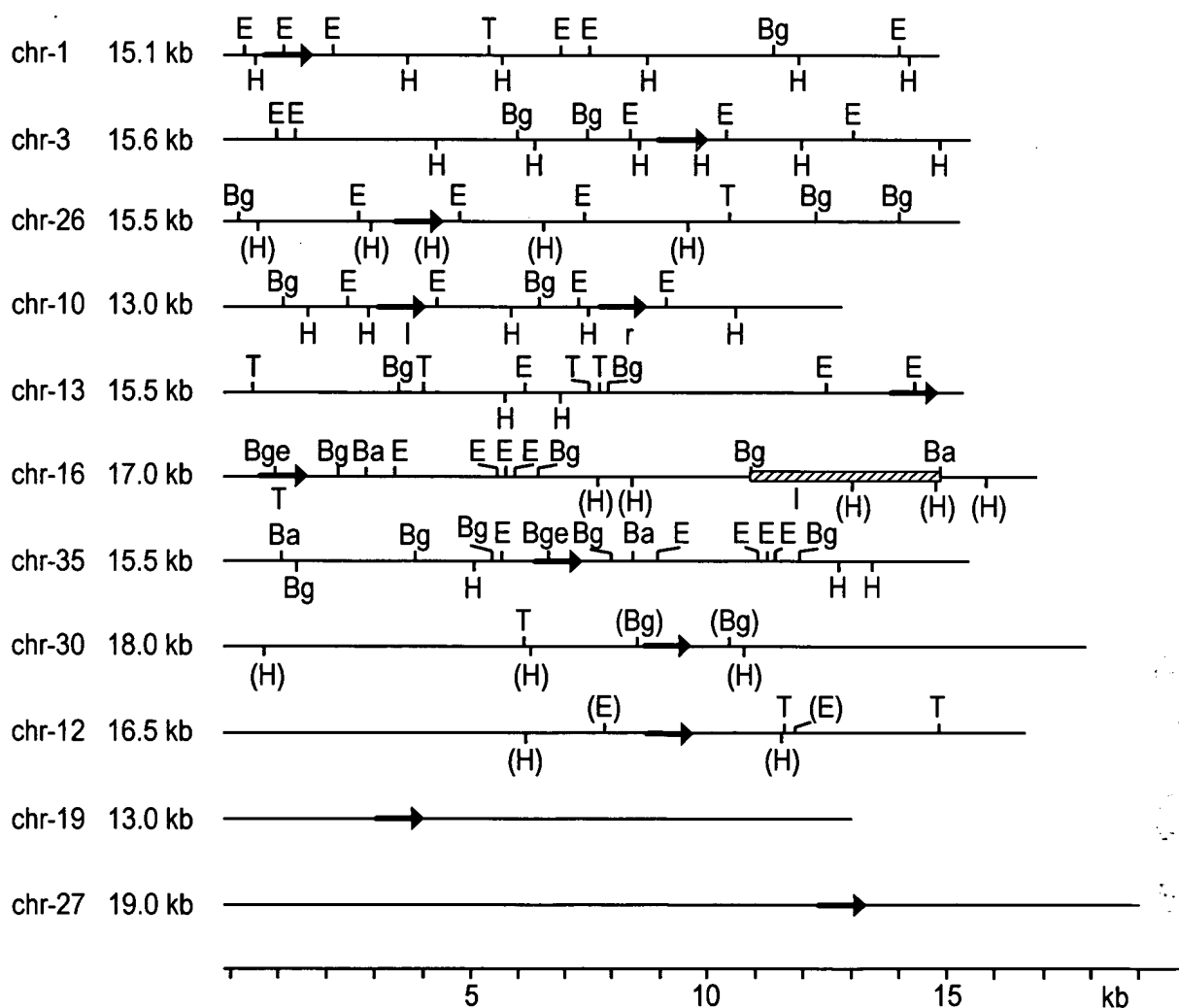






## FIG. 18

### PARTIAL RESTRICTION MAPS OF CLONED, IFN- $\alpha$ RELATED CHROMOSOMAL DNA SEGMENTS



E: Eco RI, Ba: Bam HI, Bg: Bgl II, Hinc III, T: Tac I

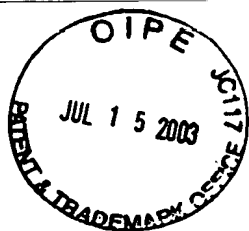
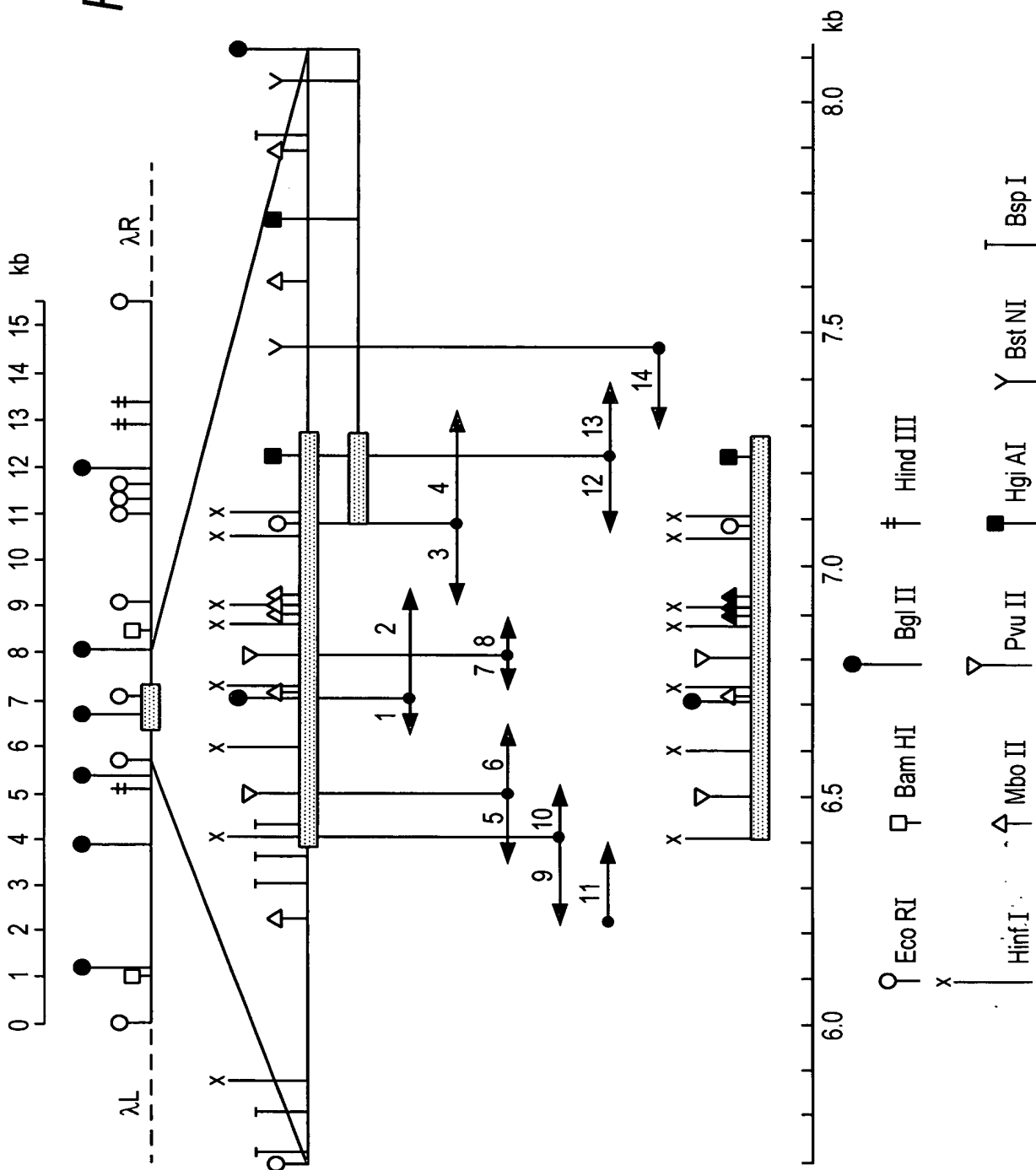
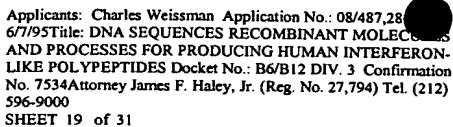


FIG. 19





AAAAACAAAACATTTGAGAAACACGGCTCTAAACTCATGTAAAGAGTGCATGAAGGAAAGCAAAAACAGAAATG

GAAAGTGGCCAGAGCATTAGAAAGTGGAAATCAGTATGTTCCCTATTTAAGGCATTTGCAGGAAGCAAGGCCTTCAGAGAACCTAGA  
 -140 -120 -100 -80 -60  
 Bsp I Bsp I

S10  
 S1  
 +1  
 20  
 meta l a s e r p r o p h e a l a l e u l e u m e t m e t v a l l e u  
 -20  
 40  
 G C C C A A G G T T C A G A G T C A C C C A T C T C A G C A A G C C C A G A G T A T C T G C A A T A T C T A C G A T G G C C T C G C C C T T T G C T T T A C T G A T G G T C C T G  
 Hinf  
 Bsp I  
 Eco RII  
 Ava II

40  
 valvalleusercyslyssersercysleuglycysaspleuprogluthrhrissrleuaspasnargargthrleumetleuleu  
 60  
 S20  
 1  
 10  
 100  
 120  
 GTGGTGCTCAGCTGCAAGTCAAGCTGCTCTCTGGGCTGTGATCTCCCTGAGACCCACAGCCTGGATAACAGGAGGACCTTGATGCTCCTG  
 Dde I Pvu II Alu I Mbo I Dde I Eco PI Eco RII Ava II Sfa NI Eco RII  
 Alu I

FIG. 20

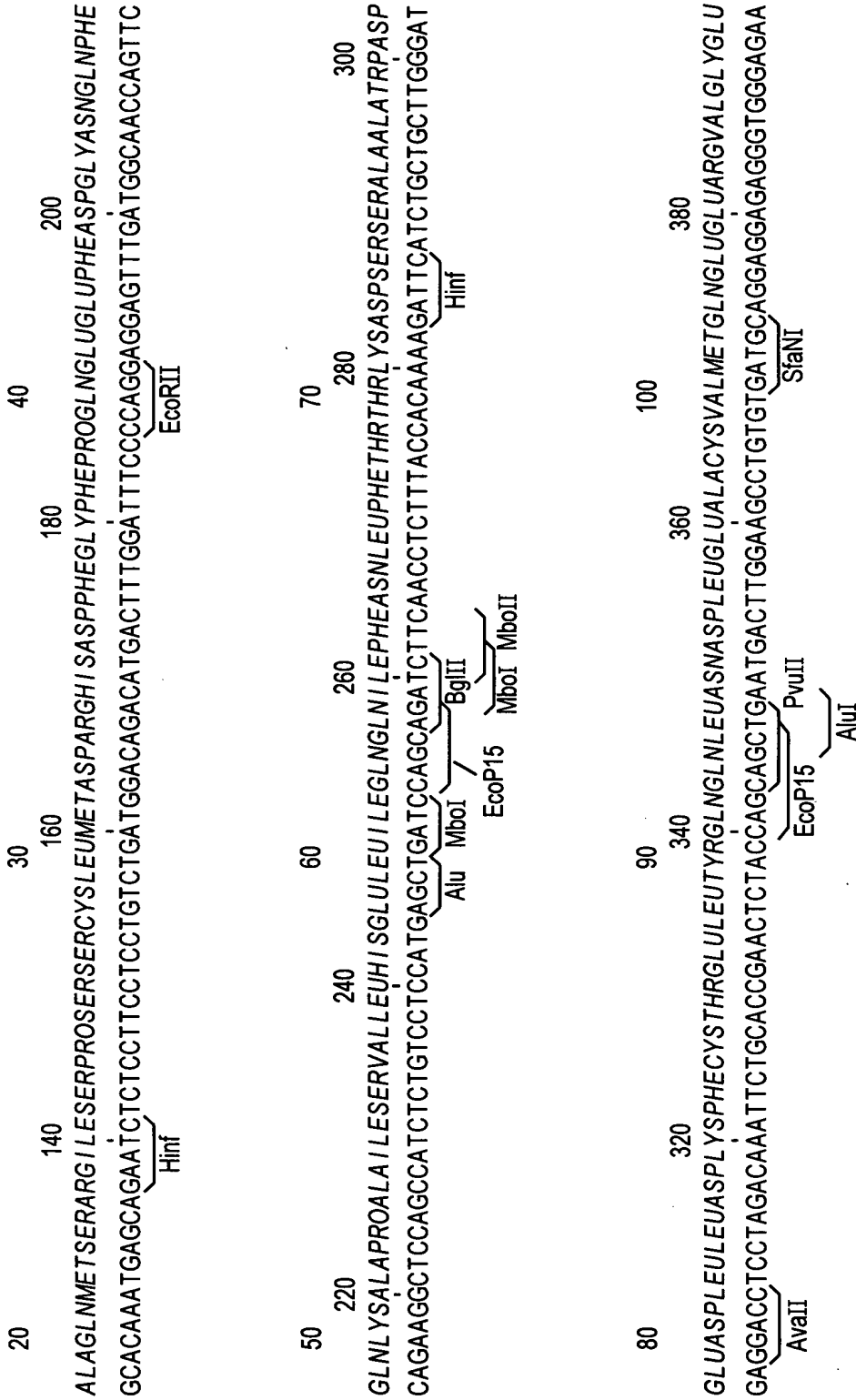


FIG. 21

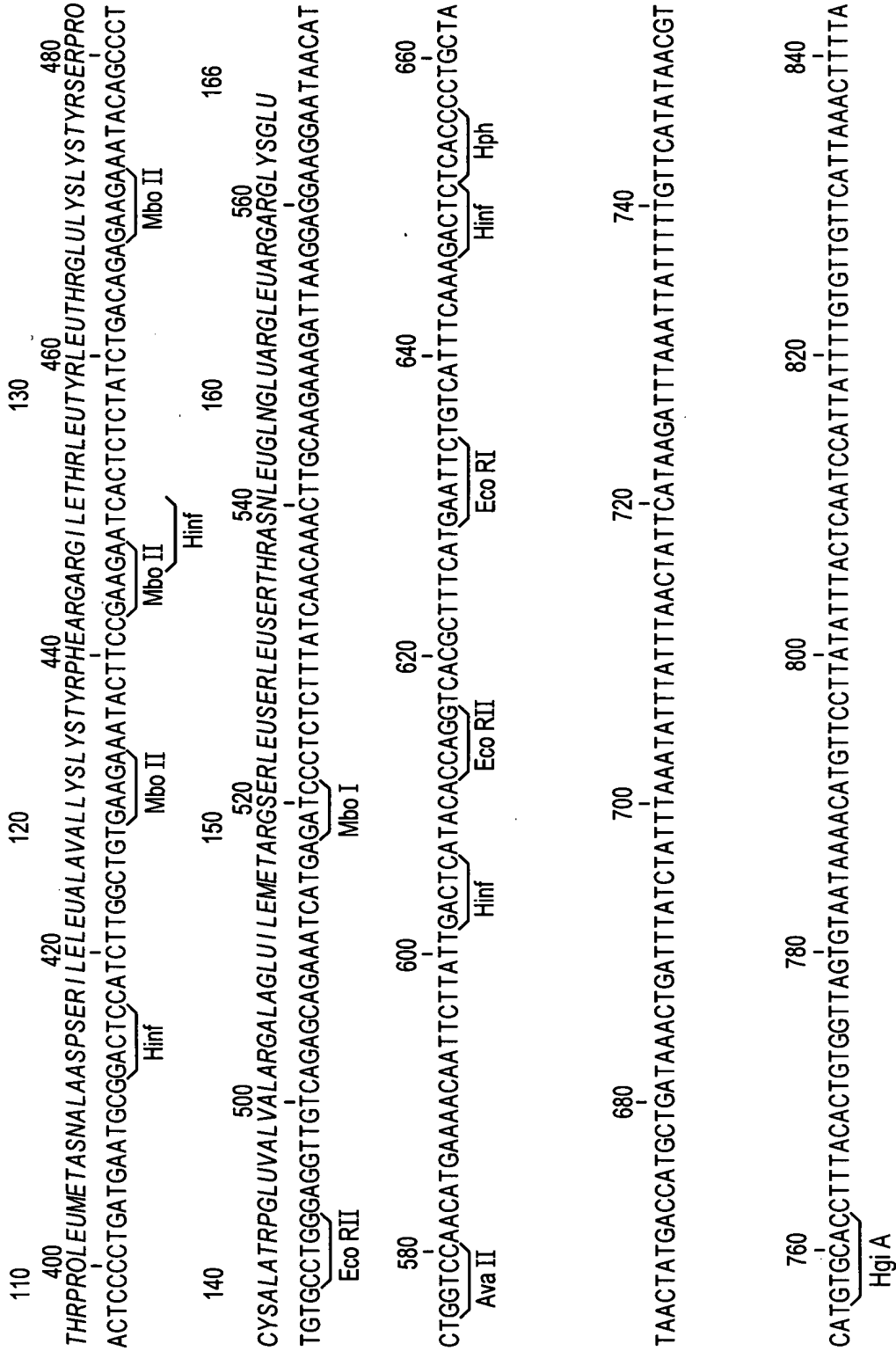


FIG. 22



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CTATAGGAACCTTCCTGTATGTGTTCATTCTTTAATATGAAATTCCTAGCCTGACTGTGCAACCTGATTAGAGAAATAAAGGGTATATTTTA  
860 920  
TTTGCTTATCATTATTATATGTAGA  
940 959

FIG. 23



### LINKAGE OF IFN- $\alpha$ RELATED GENES

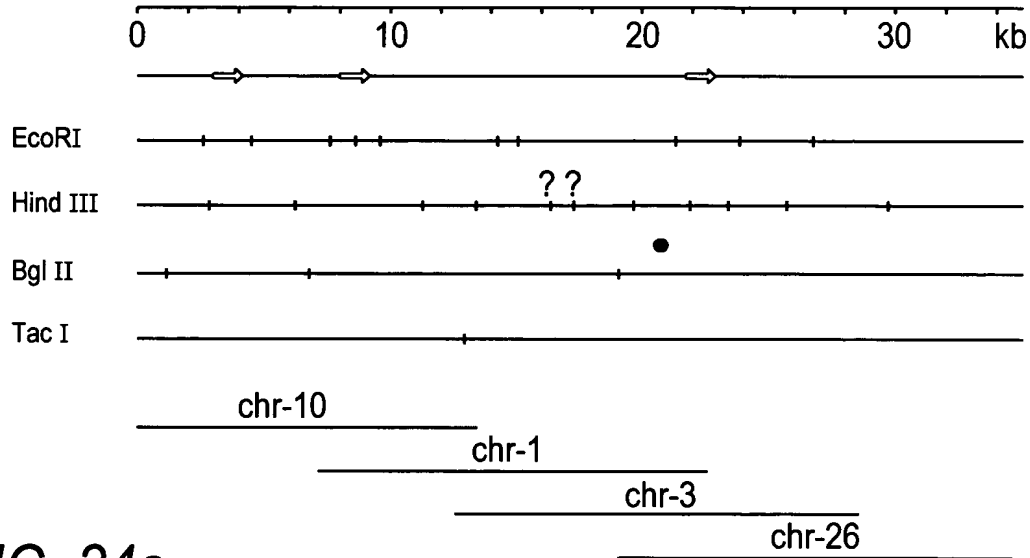


FIG. 24a

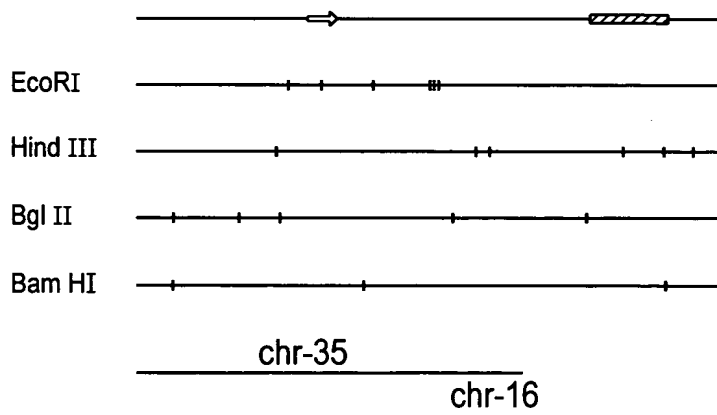


FIG. 24b



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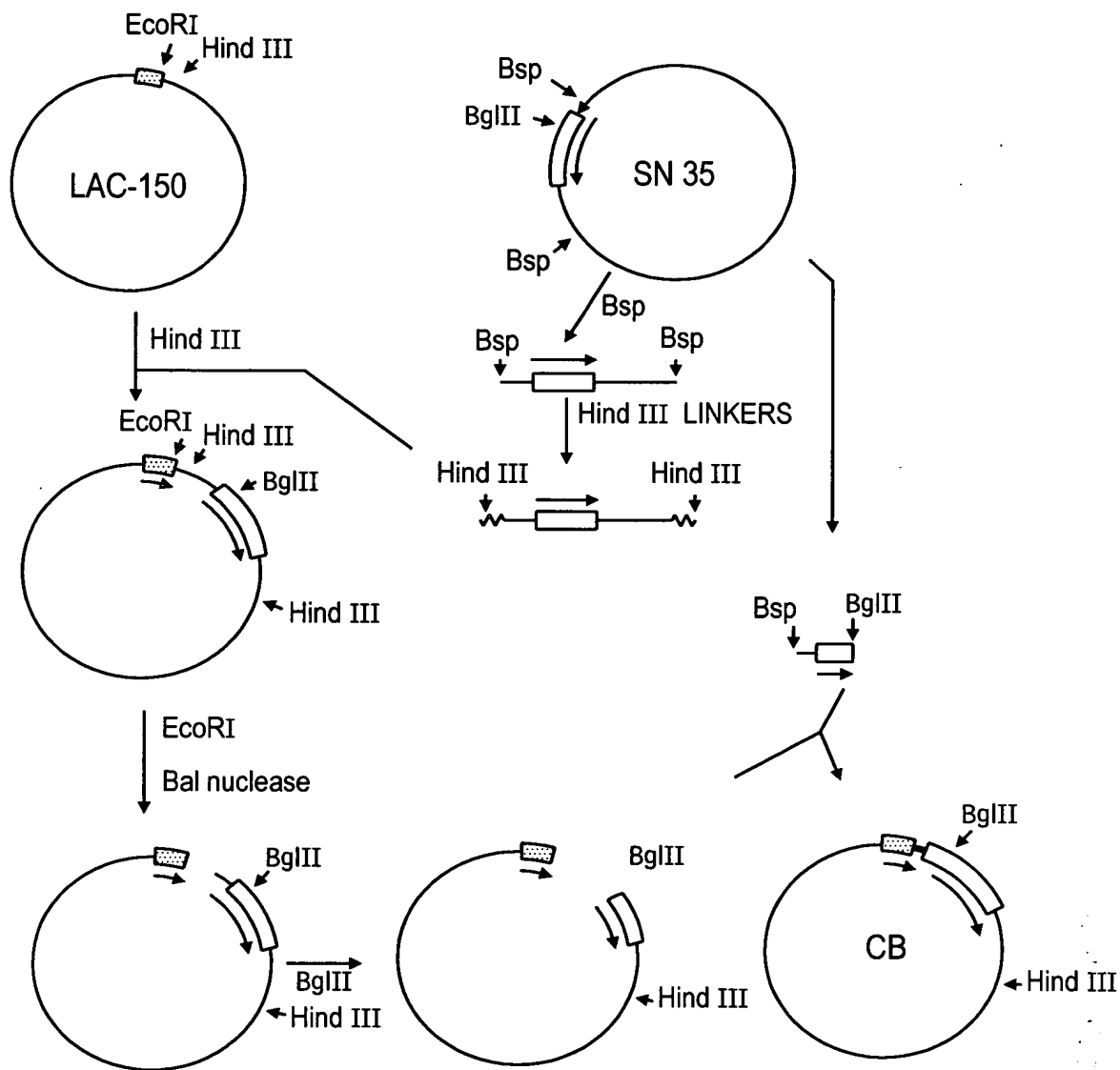


FIG. 25





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FIG. 26

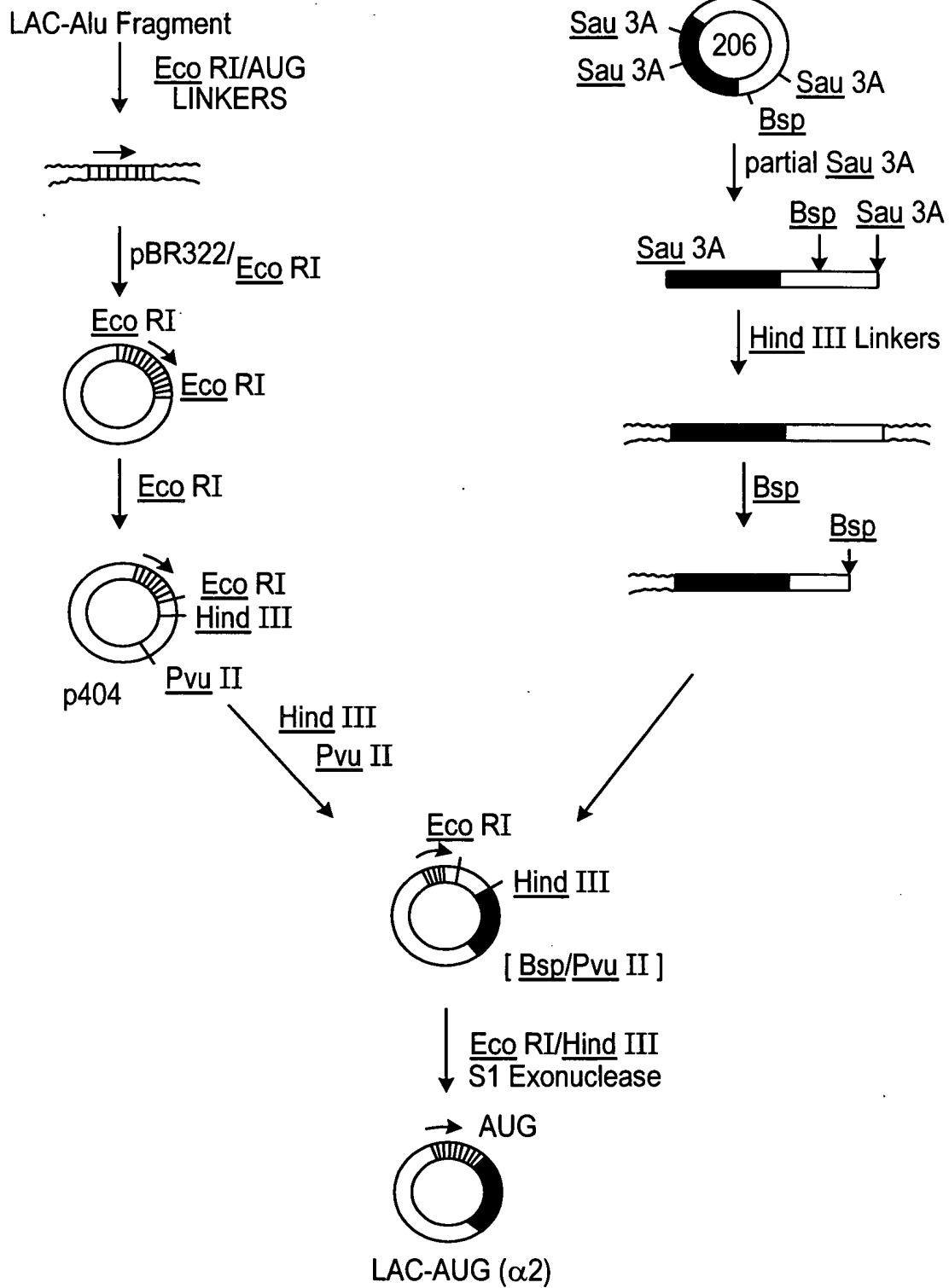
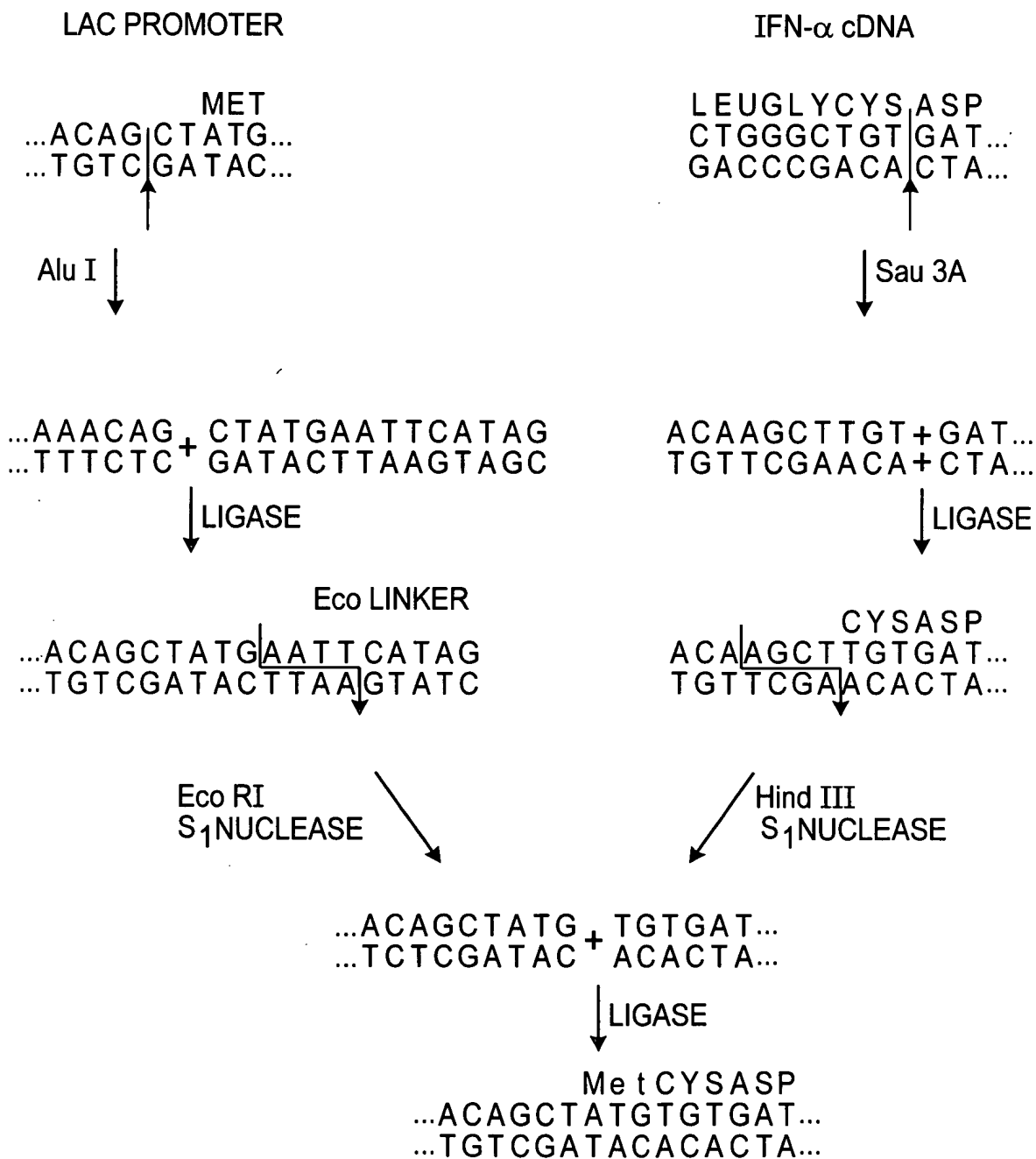




FIG. 27

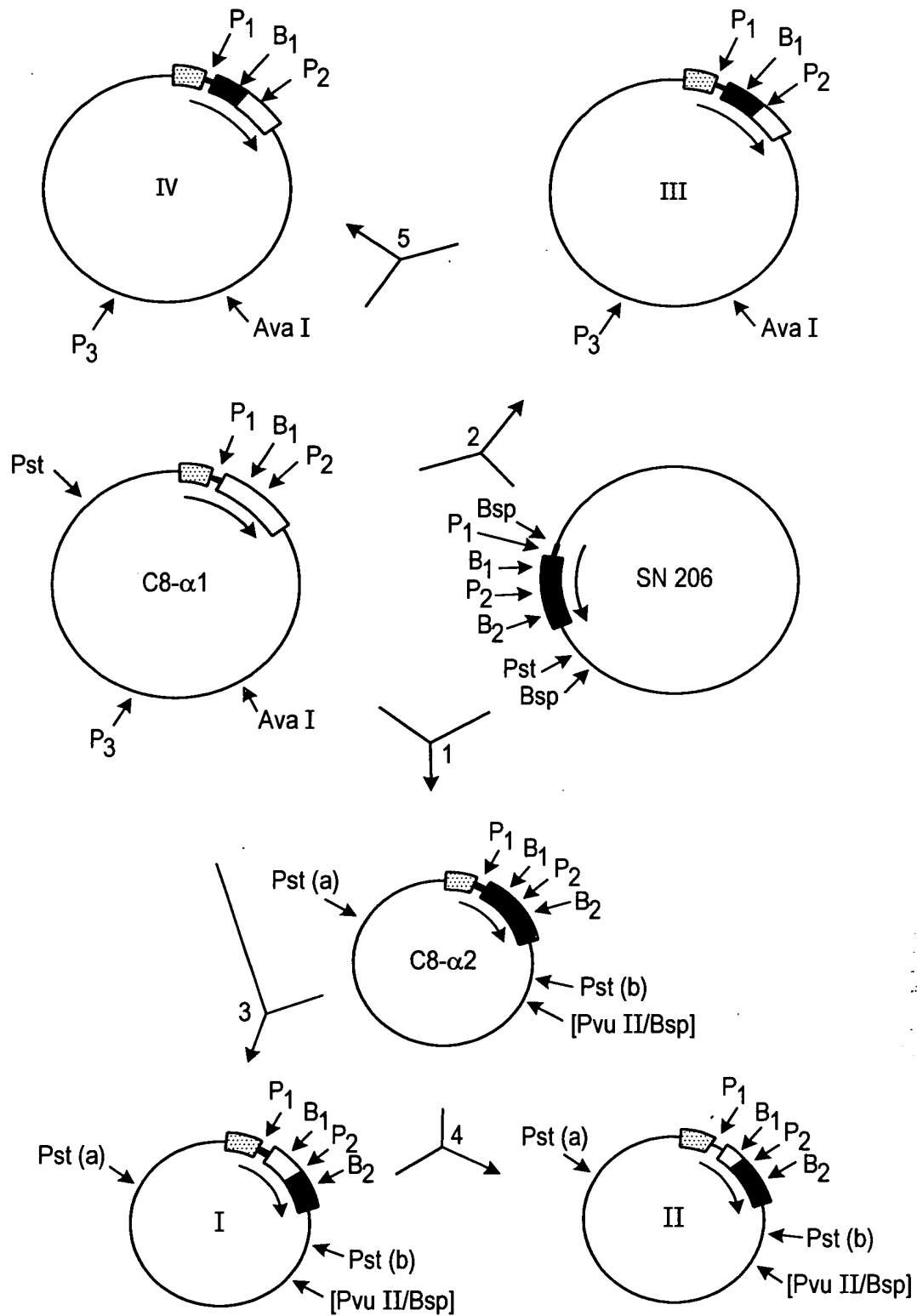
CONSTRUCTION OF PLASMID LAC-AUG( $\alpha$ -2)





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FIG. 28





160 180 200  
C<sub>24</sub>AATGCAAAATAGCTTATATATATGATTATTTCTAGTAAA  
AluI

220 240 260 280 300  
GTTATTCAACACATCAGTACCTTATGTCAACTGCTGAAAAGAAAAAGTGTGGCAACATCTGGATGAATACTGCAGCTGATGAAGTTTACAAAAATTATTTT  
RsaI ChulI PstI AluI PvuII BbsII

320 340 360 380 400  
GTCATATAAGCAAAATTCAAAGCTTCATACACTAAGAGAAAAATTTTAAAAAATTATTCATTCATATTTTAGGAGTTTGAATGATTGGATATGTAAT  
EcoRI BbrI AluI DdeI EcoRI

420 440 460 480 500  
TATATTCATATTATTAATGTGTATCTATATAGATTTTATTTTGCATATGTACTTTTGATACAAAAATTTACATGAACAAATTACACTAAAGTTATTCACACA  
EcoRI RsaI EcoRI

520 540 560 580 600  
ATATACTTATCAAAATTAAGTTAATGTCAATAGCTTTTAAACTTAAATTTTAGTTTAGTACCTTTCTGTCACTTCTACTTACTTTGAATAAAAAAGAGCA  
AluI EcoRI AluI

FIG. 29

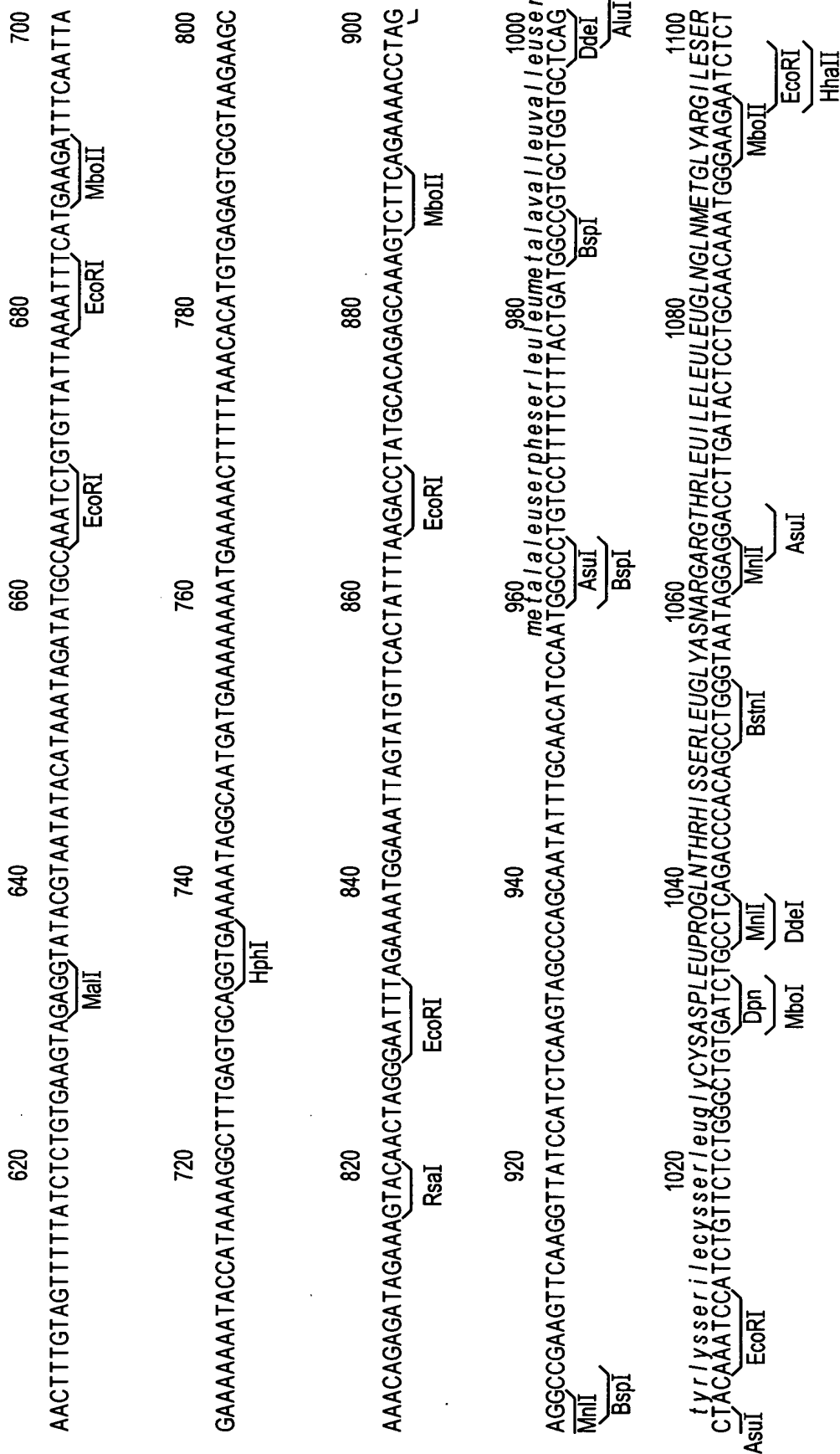
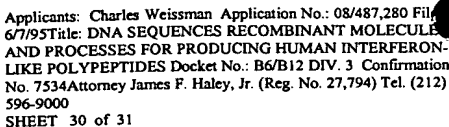


FIG. 30



1120  
H I S P H E S E R C Y S L E U L Y S A S P A R G H I S A S P P H E G L Y P H E P R O G L U G L U P H E A S P G L Y H I S G L N P H E G L N L Y S T H R G L N A L A I L E S E R V A L L E U H I S  
C A T T T C T C C T G C C T G A A G G A C A G A C A T G A T T C G G A T T C C C G A G G A G G A T T G A T G C C A C C A G T T C C A G A A G A C T C A A G C C A T C T C T G T C C T C C A T G

1140  
EcoRI MboII BstNI HhaI MboIII HhaI MnlI

1200  
G L U M E T I L E G L N G L N T H R P H E A S N L E U P H E S E R T H R G L U A S P S E R S E R A L A A T R P G L U G L N S E R L E U L E U G L U L Y S P H E S E R T H R G L U L E U T Y R G L N G L N  
A G A T G A T C C A G C A G A C C T T C A A T C T C T C A G C A C A G A G G A C T C A T C T G C T G C T T G G A A C A G A G C C T C C T A G A A A A T T T C C A C T G A A C T T T A C C A G C A

1240  
DpnII EcoRI MboII MnlI BbsI MnlI EcoRI HhaII

1300  
L E U A S N A S P L E U G L U A L A C Y S V A L I L E G L N G L U V A L G L Y V A L G L U G L U T H R P R O L E U M E T A S N V A L A S P S E R I L E L E U A L A V A L A R G L Y S T Y R P H E G L N  
A C T G A A T G A C C T G G A A G C A T G T G T G A T A C A G G A G G T T G G G T G G A A G A G A C T C C C C T G A T G A A T G T G G A C T C C A T C C T G G C T G T G A G G A A A T A C T T C C A A

1340  
BstNI MnlI MboII HhaII BstNI MnlI

1400  
A R G I L E T H R L E U T Y R L E U T H R G L U L Y S L Y S T Y R S E R P R O C Y S A L A T R P G L U V A L V A L A R G A L A G L U I L E M E T A R G S E R L E U S E R P H E S E R T H R A S N L E U  
A G A A T C A C T C T T T A T C T A A C A G A G A A G A A A T A C A G C C C T T G T G C C T G G G A G G T T G C A G A G C A G A A A T C A T G A T C C C T C T C G T T T C A C A A A C T T G C

1440  
HhaII MboII BstNI MnlI BstNI DpnII MnlI

1500  
G L N L Y S A R G L E U A R G A R G L Y S A S P  
A A A A A G A T T A A G G A G G A G G A T T G A A A C C T G G T T C A A C A T G G A A A T G A T T C C G A C T G A C T A A T A C A T T A T C T C A C A C T T T C A T G A G T T C T T C C A T T T C A

1540  
MnlI BstNI HhaII MboII

1600



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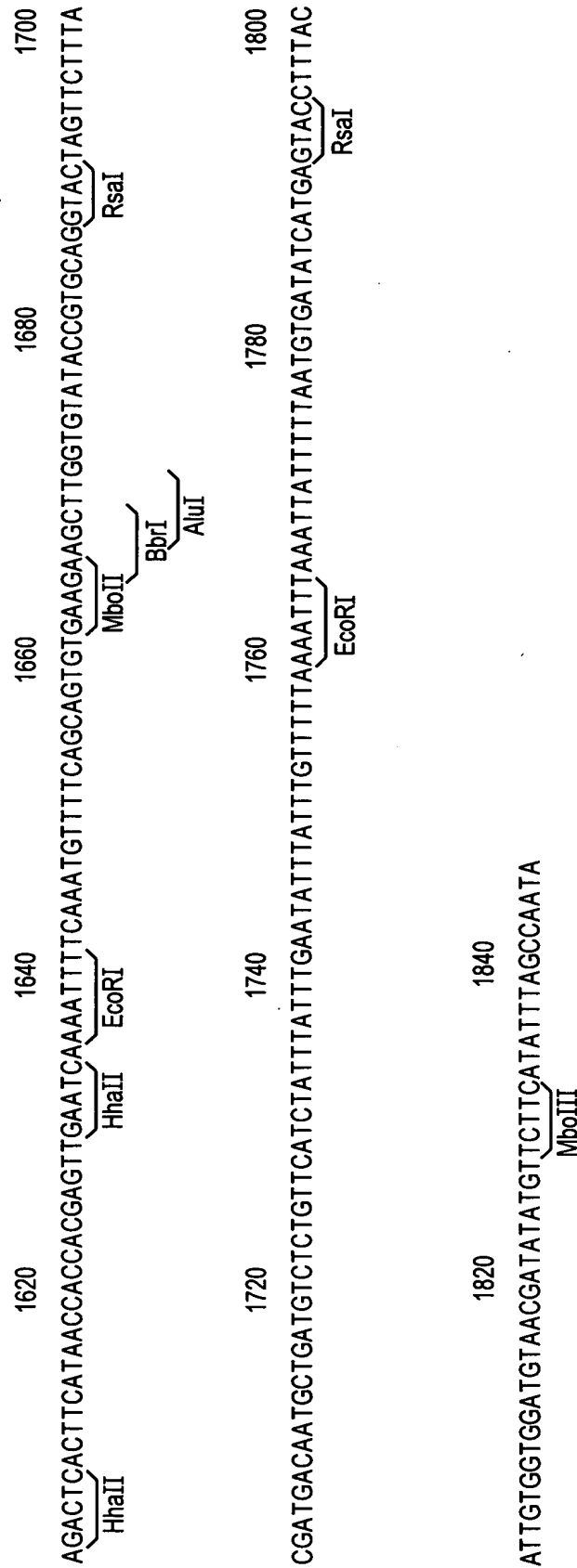


FIG. 32